

Quality: 1772.00 Length: 335  
Ratio: 5.290 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-745-605-4 x AAZ49571 ..

Align seg 1/1 to: AAZ49571 from: 1 to: 1008

1 MetAlaGlySerProThrCysLeuThrLeuIleTyrIleLeuTrpGlnLe 17  
1 ATGGCTGGTTCCTCCCAACATGCTCACCCTCATCTATATCTTTGGCAGCT 50  
17 uThrGlySerAlaAlaSerGlyProValLysGluLeuValGlySerValG 34  
51 CACAGGGTCAGCAGCCTCTGGACCCGTGAAGAGAGCTGGTCCGTTG 100  
34 lyGlyAlaValThrPheProLeuLysSerLysValLysGlnValaspSer 50  
101 GTGGGGCCGTGACTTTCCCTGAGTCCCAAGTAAAGCAAGTACTCT 150  
51 IleValTrpThrPheAsnThrThrProLeuValThrIleGlnProGluG 67  
151 ATGTCTGTGACCTTCAACACACACCCCTCTTGTGACCATACAGCCAGAAG 200  
67 yGlyThrIleIleValThrGlnAsnArgAsnArgGluArgValaspPheP 84  
201 GGGCACTATCATAGTGACCCCAAAATCGTAATAGGAGAGAGTAGACTTCC 250  
84 roAspGlyGlyTyrSerLeuLysLeuSerLysLysLysLysAsnAspSer 100  
251 CAGATGGAGGCTACTCCCTGAGCTCAGCAAACTGAAGAAGAAATGACTCA 300  
101 GlyIleTyrThrValGlyIleTyrSerSerSerSerLeuGlnGlnProSerTh 117  
301 GGGATCTACTATGTGGGATATACAGCTCATCACTACTCCAGCAGCCCTCCAC 350  
117 rGlnGluTyrValLeuHisValTyrGluHisLeuSerLysProLysValT 134  
351 CCAGGAGTACGTGCTGCTACGAGCACCTGTCAAGCCCTAAAGTCA 400  
134 hrMetGlyLeuGlnSerAsnLysAsnGlyThrCysValThrAsnLeuThr 150  
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451 TGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTTGAAGGCCCT 500  
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501 GGGGCAAGCAGCAATGAGTCCCAATAGTGGTCCATCTCCCTCCCTCTCT 550  
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217 yAlaAlaAspAspProAspSerSerMetValLeuLeuCysLeuLeuLeu 234  
651 TGCTGCTGATGACCCAGATTCCTCCATGGTCTCTCTCTCTCTCTCTCT 700  
234 alProLeuLeuSerLeuPheValIleuGlyLeuPheLeuTrpPheLeu 250  
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267 eCysArgGluThrProAsnIleCysProHisSerGlyGluAsnThrGluT 284  
801 TTGTCGGGAAACTCTTAACATATGCCCATATCTTGGAGAGAACACAGAGT 850  
284 yrAspThrIleProHisThrAsnArgThrIleLeuLysGluAspProAla 300  
851 ACGACACAAATCCCTCACACTAATAGAACAAATCTAAAGGAAGATCCAGCA 900  
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901 AATACGGTTTACTCCACTGTGGAATATCCGAAAGATGGAAATATCCCA 950  
317 sSerLeuLeuThrMetProAspThrProArgLeuPheAlaTyrGluAsnV 334  
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XX  
AC AAZ65040;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1138 encoding cdna.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
OS Homo sapiens.  
XX  
PN WO9963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
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PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
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1 MetAlaGlySerProThrCysLeuThrLeuIleTyrIleLeuTrpGlnLe 17  
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34 lyGlyAlaValThrPheProLeuLysSerLysValLysGlnValAspSer 50  
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67 yGlyThrIleIleValThrGlnAsnArgAsnArgGluArgValAspPhe 84  
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101 GlyIleTyrTyrValGlyIleTyrSerSerSerLeuGlnGlnProSerTh 117  
338 GGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAGCCCTCCAC 387  
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388 CCAGGAGTACGTGCTGCTACGAGCAGCTGTCAAGACCTAAAGTCA 437  
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438 CCATGGGTCTGCAGAGCAATAAGATGGCACCTGTGTGACCAATCTGACA 487  
151 CysCysMetGluHisGlyGluGluAspValIleTyrThrTrpLysAlaLe 167  
488 TGCTGCATGGAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCT 537  
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588 GGAGATGGGAGAAAGTGATATGACCTTCTCTGCTGCTGCTGCTGCTGCT 637  
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638 GTCAGCAGAAACTTCTCAAGCCCATCTCTGCTGCTGCTGCTGCTGCTGCT 687  
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DT 15-MAY-2001 (first entry)  
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KW Human; PRO protein; mapping; ss.  
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OS Homo sapiens.  
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PN WO200116318-A2.  
XX  
PD 08-MAR-2001.  
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PF 24-AUG-2000; 2000WO-US23328.  
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PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 07-DEC-1999; 99US-0169495.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 03-MAR-2000; 2000US-0187202.  
PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 05-JUN-2000; 2000US-0209832.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX  
DR WPI; 2001-183260/18.  
DR P-PSDB; AAB87548.  
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PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
XX chromosome and gene mapping.  
PS Claim 2; Fig 45; 278pp; English.  
XX  
CC The present sequence is the coding sequence for a human PRO polypeptide  
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
CC antagonists or anti-PRO antibodies are useful for preparation of a  
CC medicament useful in the treatment of a condition which is responsive to  
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
CC protein may also be employed as molecular weight markers for protein  
CC electrophoresis. The PRO coding sequence has applications in molecular  
CC biology, including use as hybridisation probes, and in chromosome and  
XX gene mapping.  
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 other;

Query Match 10.1%; Score 272; DB 10; Length 332;  
Best Local Similarity 99.7%; Pred. No. 3.3e-54;  
Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2328 aacaaacacacctgtgtaggtcagtggtgacgtgaagatgaacatccctaccacac 2387  
Db 263 AACRAACAACACCTGTGTAGGTGCTAGTCTGGCAGCTAAGATGAACATCCCTACCAACAC 204  
QY 2388 agagctcaccatctcttatacttaagtgaacacatggggaaggggaaatggct 2447  
Db 203 AGAGCTCACCATCTCTTACTTAAAGTGAACAAACATGGGGAAGGGGAATGGCT 144  
QY 2448 gctttgatattgtccctgacgcatacttgaatggagacccctccctaccacagtgatgaaa 2507  
Db 143 GCTTTGATATGTTCCCTGACACATATCTTGAATGGAGACCTCCCTACCAAGTGATGAAA 84  
QY 2508 gtgtgaaaaaacttaataacaaatgctgttggtggaagaatgggattgagattatcttc 2567  
Db 83 GTGTGAAAAAAGCTTAATAACAAATGCTTGTGGCAAGAATGGGATGGAGATTATCTTC 24  
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Db 23 TCTCAGAAAGGCATTGTGAAGGA 1

RESULT 32  
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LOCUS  
DEFINITION UI-H-B11-aep-d-12-0-UI.s1 NCI\_CGAP\_Sub3 Homo sapiens cDNA clone  
IMAGE:2719943 3', mRNA sequence.

ACCESSION AW138797  
VERSION AW138797.1 GI:6143115  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 557)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html The following repetitive  
elements were found in this cDNA sequence: 67-112,  
>MER31A#LTR/MER4-group  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2719943"  
/clone\_lib="NCI\_CGAP\_Sub3"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT730-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not 1; Site 2: Eco RI; The  
NCI\_CGAP\_Sub3 library is a subtracted library derived from  
the NCI\_CGAP\_Sub1 library, which is a subtracted library  
derived from BI. BI constitutes a mixture of 21

normalized or subtracted NCI\_CGAP libraries: NCI\_CGAP\_Co4  
, NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_Co10,  
NCI\_CGAP\_Co16, NCI\_CGAP\_Kid5, NCI\_CGAP\_Kid12,  
NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2,  
NCI\_CGAP\_Br2, NCI\_CGAP\_Co8, NCI\_CGAP\_CLL1, NCI\_CGAP\_Le12,  
NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24,  
NCI\_CGAP\_Lu19, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6,  
NCI\_CGAP\_Brn25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with  
a driver whose composition is detailed below:  
NCI\_CGAP\_Kid3 pool 1 LLAM 3334-3337, 3682-3683,  
3798-3803 (IMAGE Clones 1322376-1323911, 1456008-1456775  
, 1500552-1502855); NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342  
, 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831,  
1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1  
LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991,  
1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,  
1469064-1470983, 1475592-1476743); NCI\_CGAP\_Pr22 pool 1  
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones  
985608-986759, 1101192-1101959, 1217928-1220615);  
NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
Clones 1057416-1061255, 1144584-1145351). Subtraction  
was performed as previously described [Bonaldo, Lennon &  
Soares (1996): Normalization and Subtraction: Two  
Approaches To Facilitate Gene Discovery. Genome Research  
6, 791-806.

TAG LIB=NCI\_CGAP\_Le12  
TAG\_TISSUE=lelomyosarcoma  
TAG\_SEQ=AATCG

BASE COUNT 142 a 112 c 116 g 187 t  
ORIGIN

Query Match 9.9%; Score 267; DB 10; Length 557;  
Best Local Similarity 99.7%; Pred. No. 2.9e-53;  
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2382 caacacagagctcacatctcttatacttaagtgaacacatggggaaggggaagggga 2441  
Db 318 CAACACAGAGCTCACATCTCTTATCTTAAGTGAAAAACATGGGGAAGGGGAAGGGGA 259  
QY 2442 atggctgttttgatgttccctgacgcatacttgaatggagacccctccctaccagt 2501  
Db 258 ATGGCTGCTTTTGATGTGTTCCCTGACACATATCTTGAATGGAGACCTCCCTACCAAGTG 199  
QY 2502 atgaaagtgttgaacaaacttaataacaaatgctgttggcagaagatgggattgagatt 2561  
Db 198 ATGAAAGTGTGAAAAAAGCTTAATAACAAATGCTTGTGGCAAGAATGGGATGGAGATT 139  
QY 2562 atcttctcagaagagcattgtggaaggaattgagccagatctctccctactgcaaaa 2621  
Db 138 ATCTTCTCTCAGAAAGGCATTGTGGAAGGAATTGAGCCAGATCTCTCTCTCTACTGCAAAA 79  
QY 2622 ccctattgtagtaaaaaagtctcttactatcttaataaaacagatatgtgagattca 2681  
Db 78 CCTATTGTAGTAAAAAGTCTCTTACTATCTTAATAAAACAGATATTGTGAGATTCA 19  
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Db 18 CATAAAAAAGAAAAA 1

RESULT 33  
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LOCUS  
DEFINITION H73135 436 bp mRNA EST 31-OCT-1995  
IMAGE:232739 5', mRNA sequence.  
ACCESSION H73135  
VERSION H73135.1 GI:1046989  
KEYWORDS EST.  
SOURCE human.





US 097456050KP1



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Dossier: 09745605

Legal Date: 24-05-2002

| No. | Doccode | Number of pages |
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| 1   | SRNT    | 2               |

Total number of pages: 2

Remarks:

Order of re-scan issued on .....